



## SEQUENCE LISTING

<110> DeBonte, Lorin R.  
Fan, Zhegong  
Miao, Guo-Hua

<120> FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF

<130> 07148-063003

<140> US 09/771,904

<141> 2001-01-29

<150> US 08/874,109

<151> 1997-06-12

<160> 70

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1155

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)...(1152)

<223> Wild type Fad2

<221> misc\_feature

<222> 205

<223> n = a, g, c, or t/u

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gaa acc gac acc atc aag cgc gta ccc tgc gag aca ccg ccc ttc act 96  
Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr  
20 25 30

gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg 144  
Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser  
35 40 45

atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc 192  
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser  
50 55 60

tgc ttc tac tac ntc gcc acc act tac ttc cct ctc ctc cct cac cct 240  
Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro

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ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc caa ggg tgc gtc				288
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val				
	85	90	95	
cta acc ggc gtc tgg gtc ata gcc cac gaa tgc ggc cac cac gcc ttc				336
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe				
	100	105	110	
agc gac tac cag tgg ctt gac gac acc gtc ggt ctc atc ttc cac tcc				384
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser				
	115	120	125	
ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cgc agc cac				432
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His				
	130	135	140	
cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag				480
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys				
	145	150	155	160
aag aag tca gac atc aag tgg tac ggc aag tac ctc aac aac cct ttg				528
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu				
	165	170	175	
gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg ccg ttg				576
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu				
	180	185	190	
tac tta gcc ttc aac gtc tcg gga aga cct tac gac ggc ggc ttc cgt				624
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg				
	195	200	205	
tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgc gag cgt ctc				672
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu				
	210	215	220	
cag ata tac atc tcc gac gct ggc atc ctc gcc gtc tgc tac ggt ctc				720
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu				
	225	230	235	240
ttc cgt tac gcc gcc ggc cag gga gtg gcc tcg atg gtc tgc ttc tac				768
Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr				
	245	250	255	
gga gtc ccg ctt ctg att gtc aat ggt ttc ctc gtg ttg atc act tac				816
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr				
	260	265	270	
ttg cag cac acg cat cct tcc ctg cct cac tac gat tcg tcc gag tgg				864
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp				
	275	280	285	

gat tgg ttc agg gga gct ttg gct acc gtt gac aga gac tac gga atc	912
Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile	
290 295 300	

ttg aac aag gtc ttc cac aat att acc gac acg cac gtg gcc cat cat	960
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	
305 310 315 320	

ccg ttc tcc acg atg ccg cat tat cac gcg atg gaa gct acc aag gcg	1008
Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala	
325 330 335	

ata aag ccg ata ctg gga gag tat tat cag ttc gat ggg acg ccg gtg	1056
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val	
340 345 350	

gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg	1104
Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro	
355 360 365	

gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta	1152
Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu	
370 375 380	

tga	1155
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<210> 2

<211> 384

<212> PRT

<213> Brassica napus

<220>

<223> Xaa = Phe, Leu, Ile, or Val

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35 40 45	
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser	
50 55 60	
Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro	
65 70 75 80	
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val	
85 90 95	
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe	
100 105 110	
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser	
115 120 125	
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His	
130 135 140	

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys  
 145 150 155 160  
 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu  
 165 170 175  
 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu  
 180 185 190  
 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg  
 195 200 205  
 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu  
 210 215 220  
 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu  
 225 230 235 240  
 Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr  
 245 250 255  
 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr  
 260 265 270  
 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp  
 275 280 285  
 Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile  
 290 295 300  
 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His  
 305 310 315 320  
 Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala  
 325 330 335  
 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val  
 340 345 350  
 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro  
 355 360 365  
 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu  
 370 375 380

<210> 3

<211> 1155

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)...(1152)

<223> G to A transversion mutation at nucleotide 316

<221> misc\_feature

<222> 205

<223> n = a, g, c, or t/u

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 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser  
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48

gaa acc gac acc atc aag cgc gta ccc tgc gag aca ccg ccc ttc act  
 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr  
 20 25 30

96

gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser 35 40 45	144
atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser 50 55 60	192
tgc ttc tac tac ntc gcc acc act tac ttc cct ctc ctc cct cac cct Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro 65 70 75 80	240
ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc caa ggg tgc gtc Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val 85 90 95	288
cta acc ggc gtc tgg gtc ata gcc cac aag tgc ggc cac cac gcc ttc Leu Thr Gly Val Trp Val Ile Ala His Lys Cys Gly His His Ala Phe 100 105 110	336
agc gac tac cag tgg ctt gac gac acc gtc ggt ctc atc ttc cac tcc Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser 115 120 125	384
ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cgc agc cac Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His 130 135 140	432
cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys 145 150 155 160	480
aag aag tca gac atc aag tgg tac ggc aag tac ctc aac aac cct ttg Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu 165 170 175	528
gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg ccg ttg Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu 180 185 190	576
tac tta gcc ttc aac gtc tcg gga aga cct tac gac ggc ggc ttc cgt Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg 195 200 205	624
tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgc gag cgt ctc Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu 210 215 220	672
cag ata tac atc tcc gac gct ggc atc ctc gcc gtc tgc tac ggt ctc Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu 225 230 235 240	720

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Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr	
245 250 255	

gga gtc ccg ctt ctg att gtc aat ggt ttc ctc gtg ttg atc act tac	816
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr	
260 265 270	

ttg cag cac acg cat cct tcc ctg cct cac tac gat tcg tcc gag tgg	864
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp	
275 280 285	

gat tgg ttc agg gga gct ttg gct acc gtt gac aga gac tac gga atc	912
Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile	
290 295 300	

ttg aac aag gtc ttc cac aat att acc gac acg cac gtg gcc cat cat	960
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	
305 310 315 320	

ccg ttc tcc acg atg ccg cat tat cac gcg atg gaa gct acc aag gcg	1008
Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala	
325 330 335	

ata aag ccg ata ctg gga gag tat tat cag ttc gat ggg acg ccg gtg	1056
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val	
340 345 350	

gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg	1104
Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro	
355 360 365	

gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta	1152
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tga	1155
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<210> 4

<211> 384

<212> PRT

<213> Brassica napus

<220>

<223> Xaa = Phe, Leu, Ile, or Val

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20 25 30	
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35 40 45	

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Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
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Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
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Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
                      85                      90                      95
Leu Thr Gly Val Trp Val Ile Ala His Lys Cys Gly His His Ala Phe
          100                      105                      110
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
          115                      120                      125
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His
          130                      135                      140
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
145                      150                      155                      160
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
          165                      170                      175
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
          180                      185                      190
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg
          195                      200                      205
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
          210                      215                      220
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
225                      230                      235                      240
Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr
          245                      250                      255
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
          260                      265                      270
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
          275                      280                      285
Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
          290                      295                      300
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
305                      310                      315                      320
Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
          325                      330                      335
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
          340                      345                      350
Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
          355                      360                      365
Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
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<210> 5

<211> 1155

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)...(1152)

<223> Wild type Fad2

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gaa acc gac aac atc aag cgc gta ccc tgc gag aca ccg ccc ttc act																	96
Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr																	
					20					25					30		
gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg																	144
Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser																	
					35					40					45		
atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc																	192
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser																	
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tgc ttc tac tac gtc gcc acc act tac ttc cct ctc ctc cct cac cct																	240
Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro																	
					65					70					75		
ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc cag ggc tgc gtc																	288
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val																	
					85					90					95		
cta acc ggc gtc tgg gtc ata gcc cac gag tgc ggc cac cac gcc ttc																	336
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe																	
					100					105					110		
agc gac tac cag tgg ctg gac gac acc gtc ggc ctc atc ttc cac tcc																	384
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser																	
					115					120					125		
ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cga cgc cac																	432
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His																	
					130					135					140		
cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag																	480
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys																	
					145					150					155		
aag aag tca gac atc aag tgg tac ggc aag tac ctc aac aac cct ttg																	528
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu																	
					165					170					175		
gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg cct ttg																	576
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu																	
					180					185					190		
tac tta gcc ttc aac gtc tcg ggg aga cct tac gac ggc ggc ttc gct																	624
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala																	
					195					200					205		



tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgc gag cgt ctc	672
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu	
210 215 220	
cag ata tac atc tcc gac gct ggc atc ctc gcc gtc tgc tac ggt ctc	720
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	
225 230 235 240	
tac cgc tac gct gct gtc caa gga gtt gcc tcg atg gtc tgc ttc tac	768
Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr	
245 250 255	
gga gtt ccg ctt ctg att gtc aat ggg ttc tta gtt ttg atc act tac	816
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr	
260 265 270	
ttg cag cac acg cat cct tcc ctg cct cac tat gac tcg tct gag tgg	864
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp	
275 280 285	
gat tgg ttg agg gga gct ttg gcc acc gtt gac aga gac tac gga atc	912
Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile	
290 295 300	
ttg aac aag gtc ttc cac aat atc acg gac acg cac gtg gcg cat cac	960
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	
305 310 315 320	
ctg ttc tcg acc atg ccg cat tat cat gcg atg gaa gct acg aag gcg	1008
Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala	
325 330 335	
ata aag ccg ata ctg gga gag tat tat cag ttg cat ggg acg ccg gtg	1056
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Leu His Gly Thr Pro Val	
340 345 350	
gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg	1104
Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro	
355 360 365	
gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta	1152
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tga	1155
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<213> Brassica napus	
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Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser						
	35			40		45
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser						
	50			55		60
Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro						
	65			70		75
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val						
	85			90		95
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe						
	100			105		110
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser						
	115			120		125
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His						
	130			135		140
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys						
	145			150		155
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu						
	165			170		175
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu						
	180			185		190
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala						
	195			200		205
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu						
	210			215		220
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu						
	225			230		235
Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr						
	245			250		255
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr						
	260			265		270
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp						
	275			280		285
Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile						
	290			295		300
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His						
	305			310		315
Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala						
	325			330		335
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Leu His Gly Thr Pro Val						
	340			345		350
Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro						
	355			360		365
Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu						
	370			375		380

&lt;210&gt; 7

&lt;211&gt; 1155

&lt;212&gt; DNA

&lt;213&gt; Brassica napus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1152)

&lt;223&gt; T to A transversion mutation at nucleotide 515

&lt;400&gt; 7

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 gaa acc gac aac atc aag cgc gta ccc tgc gag aca ccg ccc ttc act	96
Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr	
20 25 30	
 gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg	144
Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser	
35 40 45	
 atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc	192
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser	
50 55 60	
 tgc ttc tac tac gtc gcc acc act tac ttc cct ctc ctc cct cac cct	240
Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro	
65 70 75 80	
 ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc cag ggc tgc gtc	288
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val	
85 90 95	
 cta acc ggc gtc tgg gtc ata gcc cac gag tgc ggc cac cac gcc ttc	336
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe	
100 105 110	
 agc gac tac cag tgg ctg gac gac acc gtc ggc ctc atc ttc cac tcc	384
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser	
115 120 125	
 ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cga cgc cac	432
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His	
130 135 140	
 cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag	480
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	
145 150 155 160	
 aag aag tca gac atc aag tgg tac ggc aag tac cac aac aac cct ttg	528
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr His Asn Asn Pro Leu	
165 170 175	
 gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg cct ttg	576
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu	
180 185 190	

tac tta gcc ttc aac gtc tcg ggg aga cct tac gac ggc ggc ttc gct	624
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala	
195 200 205	
tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgc gag cgt ctc	672
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu	
210 215 220	
cag ata tac atc tcc gac gct ggc atc ctc gcc gtc tgc tac ggt ctc	720
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	
225 230 235 240	
tac cgc tac gct gct gtc caa gga gtt gcc tcg atg gtc tgc ttc tac	768
Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr	
245 250 255	
gga gtt ccg ctt ctg att gtc aat ggg ttc tta gtt ttg atc act tac	816
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr	
260 265 270	
ttg cag cac acg cat cct tcc ctg cct cac tat gac tcg tct gag tgg	864
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp	
275 280 285	
gat tgg ttg agg gga gct ttg gcc acc gtt gac aga gac tac gga atc	912
Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile	
290 295 300	
ttg aac aag gtc ttc cac aat atc acg gac acg cac gtg gcg cat cac	960
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	
305 310 315 320	
ctg ttc tcg acc atg ccg cat tat cat gcg atg gaa gct acg aag gcg	1008
Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala	
325 330 335	
ata aag ccg ata ctg gga gag tat tat cag ttg cat ggg acg ccg gtg	1056
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Leu His Gly Thr Pro Val	
340 345 350	
gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg	1104
Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro	
355 360 365	
gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta	1152
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tga	1155
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&lt;213&gt; Brassica napus

&lt;400&gt; 8

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			20					25					30		
Val	Gly	Glu	Leu	Lys	Lys	Ala	Ile	Pro	Pro	His	Cys	Phe	Lys	Arg	Ser
			35				40					45			
Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Ile	Trp	Asp	Ile	Ile	Ile	Ala	Ser
	50					55				60					
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Thr	Tyr	Phe	Pro	Leu	Leu	Pro	His	Pro
65					70				75						80
Leu	Ser	Tyr	Phe	Ala	Trp	Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys	Val
				85				90					95		
Leu	Thr	Gly	Val	Trp	Val	Ile	Ala	His	Glu	Cys	Gly	His	His	Ala	Phe
			100				105					110			
Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Leu	Ile	Phe	His	Ser
	115					120						125			
Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg	His
	130					135					140				
His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys
145					150				155						160
Lys	Lys	Ser	Asp	Ile	Lys	Trp	Tyr	Gly	Lys	Tyr	His	Asn	Asn	Pro	Leu
			165					170						175	
Gly	Arg	Thr	Val	Met	Leu	Thr	Val	Gln	Phe	Thr	Leu	Gly	Trp	Pro	Leu
			180					185					190		
Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Gly	Phe	Ala
	195					200						205			
Cys	His	Phe	His	Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu
	210					215					220				
Gln	Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu
225					230					235					240
Tyr	Arg	Tyr	Ala	Ala	Val	Gln	Gly	Val	Ala	Ser	Met	Val	Cys	Phe	Tyr
			245					250						255	
Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Gly	Phe	Leu	Val	Leu	Ile	Thr	Tyr
			260				265						270		
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp
	275					280						285			
Asp	Trp	Leu	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile
	290					295					300				
Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His
305					310					315					320
Leu	Phe	Ser	Thr	Met	Pro	His	Tyr	His	Ala	Met	Glu	Ala	Thr	Lys	Ala
			325					330						335	
Ile	Lys	Pro	Ile	Leu	Gly	Glu	Tyr	Tyr	Gln	Leu	His	Gly	Thr	Pro	Val
			340					345					350		
Val	Lys	Ala	Met	Trp	Arg	Glu	Ala	Lys	Glu	Cys	Ile	Tyr	Val	Glu	Pro
	355					360						365			
Asp	Arg	Gln	Gly	Glu	Lys	Lys	Gly	Val	Phe	Trp	Tyr	Asn	Asn	Lys	Leu
	370					375					380				

&lt;210&gt; 9

&lt;211&gt; 1155

&lt;212&gt; DNA

&lt;213&gt; Brassica napus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1152)

&lt;400&gt; 9

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Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser	
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 gaa acc gac aac atc aag cgc gta ccc tgc gag aca ccg ccc ttc act	96
Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr	
20 25 30	
 gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg	144
Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser	
35 40 45	
 atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc	192
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser	
50 55 60	
 tgc ttc tac tac gtc gcc acc act tac ttc cct ctc ctc cct cac cct	240
Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro	
65 70 75 80	
 ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc cag ggc tgc gtc	288
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val	
85 90 95	
 cta acc ggc gtc tgg gtc ata gcc cac gag tgc ggc cac cac gcc ttc	336
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe	
100 105 110	
 agc gac tac cag tgg ctg gac gac acc gtc ggc ctc atc ttc cac tcc	384
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser	
115 120 125	
 ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cga cgc cac	432
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His	
130 135 140	
 cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag	480
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	
145 150 155 160	
 aag aag tca gac atc aag tgg tac ggc aag tac ctc aac aac cct ttg	528
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu	
165 170 175	

gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg cct ttg	576
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu	
180 185 190	
tac tta gcc ttc aac gtc tcg ggg aga cct tac gac ggc ggc ttc gct	624
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala	
195 200 205	
tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgt gag cgt ctc	672
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu	
210 215 220	
cag ata tac atc tcc gac gct ggc atc ctc gcc gtc tgc tac ggt ctc	720
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	
225 230 235 240	
tac cgc tac gct gct gtc caa gga gtt gcc tcg atg gtc tgc ttc tac	768
Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr	
245 250 255	
gga gtt cct ctt ctg att gtc aac ggg ttc tta gtt ttg atc act tac	816
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr	
260 265 270	
ttg cag cac acg cat cct tcc ctg cct cac tat gac tcg tct gag tgg	864
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp	
275 280 285	
gat tgg ttg agg gga gct ttg gcc acc gtt gac aga gac tac gga atc	912
Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile	
290 295 300	
ttg aac aag gtc ttc cac aat atc acg gac acg cac gtg gcg cat cac	960
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	
305 310 315 320	
ctg ttc tcg acc atg ccg cat tat cat gcg atg gaa gct acg aag gcg	1008
Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala	
325 330 335	
ata aag ccg ata ctg gga gag tat tat cag ttc gat ggg acg ccg gtg	1056
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val	
340 345 350	
gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg	1104
Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro	
355 360 365	
gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta	1152
Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu	
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tga	1155

<210> 10  
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 <213> Brassica napus

<400> 10

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			20					25					30		
Val	Gly	Glu	Leu	Lys	Lys	Ala	Ile	Pro	Pro	His	Cys	Phe	Lys	Arg	Ser
			35				40					45			
Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Ile	Trp	Asp	Ile	Ile	Ile	Ala	Ser
	50					55				60					
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Thr	Tyr	Phe	Pro	Leu	Leu	Pro	His	Pro
65					70					75					80
Leu	Ser	Tyr	Phe	Ala	Trp	Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys	Val
				85					90					95	
Leu	Thr	Gly	Val	Trp	Val	Ile	Ala	His	Glu	Cys	Gly	His	His	Ala	Phe
			100					105						110	
Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Leu	Ile	Phe	His	Ser
	115						120						125		
Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg	His
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His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys
145					150					155					160
Lys	Lys	Ser	Asp	Ile	Lys	Trp	Tyr	Gly	Lys	Tyr	Leu	Asn	Asn	Pro	Leu
			165						170					175	
Gly	Arg	Thr	Val	Met	Leu	Thr	Val	Gln	Phe	Thr	Leu	Gly	Trp	Pro	Leu
			180					185					190		
Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Gly	Phe	Ala
	195						200					205			
Cys	His	Phe	His	Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu
	210					215					220				
Gln	Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu
225					230					235					240
Tyr	Arg	Tyr	Ala	Ala	Val	Gln	Gly	Val	Ala	Ser	Met	Val	Cys	Phe	Tyr
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			260					265					270		
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp
	275						280					285			
Asp	Trp	Leu	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile
	290					295					300				
Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His
305					310					315					320
Leu	Phe	Ser	Thr	Met	Pro	His	Tyr	His	Ala	Met	Glu	Ala	Thr	Lys	Ala
			325						330					335	
Ile	Lys	Pro	Ile	Leu	Gly	Glu	Tyr	Tyr	Gln	Phe	Asp	Gly	Thr	Pro	Val
			340					345					350		
Val	Lys	Ala	Met	Trp	Arg	Glu	Ala	Lys	Glu	Cys	Ile	Tyr	Val	Glu	Pro
	355						360					365			
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370 375 380

<210> 11  
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<220>  
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 gaa acc gac aac atc aag cgc gta ccc tgc gag aca ccg ccc ttc act	96
Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr	
20 25 30	
 gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg	144
Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser	
35 40 45	
 atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc	192
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser	
50 55 60	
 tgc ttc tac tac gtc gcc acc act tac ttc cct ctc ctc cct cac cct	240
Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro	
65 70 75 80	
 ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc cag ggc tgc gtc	288
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val	
85 90 95	
 cta acc ggc gtc tgg gtc ata gcc cac aag tgc ggc cac cac gcc ttc	336
Leu Thr Gly Val Trp Val Ile Ala His Lys Cys Gly His His Ala Phe	
100 105 110	
 agc gac tac cag tgg ctg gac gac acc gtc ggc ctc atc ttc cac tcc	384
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser	
115 120 125	
 ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cga cgc cac	432
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His	
130 135 140	
 cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag	480
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	
145 150 155 160	

aag aag tca gac atc aag tgg tac ggc aag tac ctc aac aac cct ttg	528
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu	
165 170 175	
gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg cct ttg	576
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu	
180 185 190	
tac tta gcc ttc aac gtc tcg ggg aga cct tac gac ggc ggc ttc gct	624
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala	
195 200 205	
tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgt gag cgt ctc	672
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu	
210 215 220	
cag ata tac atc tcc gac gct ggc atc ctc gcc gtc tgc tac ggt ctc	720
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	
225 230 235 240	
tac cgc tac gct gct gtc caa gga gtt gcc tcg atg gtc tgc ttc tac	768
Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr	
245 250 255	
gga gtt cct ctt ctg att gtc aac ggg ttc tta gtt ttg atc act tac	816
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr	
260 265 270	
ttg cag cac acg cat cct tcc ctg cct cac tat gac tcg tct gag tgg	864
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp	
275 280 285	
gat tgg ttg agg gga gct ttg gcc acc gtt gac aga gac tac gga atc	912
Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile	
290 295 300	
ttg aac aag gtc ttc cac aat atc acg gac acg cac gtg gcg cat cac	960
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	
305 310 315 320	
ctg ttc tcg acc atg ccg cat tat cat gcg atg gaa gct acg aag gcg	1008
Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala	
325 330 335	
ata aag ccg ata ctg gga gag tat tat cag ttc gat ggg acg ccg gtg	1056
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val	
340 345 350	
gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg	1104
Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro	
355 360 365	

gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta 1152  
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tga 1155

<210> 12

<211> 384

<212> PRT

<213> Brassica napus

<400> 12

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 35 40 45  
 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser  
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 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro  
 65 70 75 80  
 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val  
 85 90 95  
 Leu Thr Gly Val Trp Val Ile Ala His Lys Cys Gly His His Ala Phe  
 100 105 110  
 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser  
 115 120 125  
 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His  
 130 135 140  
 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys  
 145 150 155 160  
 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu  
 165 170 175  
 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu  
 180 185 190  
 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala  
 195 200 205  
 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu  
 210 215 220  
 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu  
 225 230 235 240  
 Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr  
 245 250 255  
 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr  
 260 265 270  
 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp  
 275 280 285  
 Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile  
 290 295 300  
 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His  
 305 310 315 320  
 Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala

				325					330					335			
Ile	Lys	Pro	Ile	Leu	Gly	Glu	Tyr	Tyr	Gln	Phe	Asp	Gly	Thr	Pro	Val		
			340					345					350				
Val	Lys	Ala	Met	Trp	Arg	Glu	Ala	Lys	Glu	Cys	Ile	Tyr	Val	Glu	Pro		
		355					360					365					
Asp	Arg	Gln	Gly	Glu	Lys	Lys	Gly	Val	Phe	Trp	Tyr	Asn	Asn	Lys	Leu		
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Glu	Thr	Asp	Thr	Ile	Lys	Arg	Val	Pro	Cys	Glu	Thr	Pro	Pro	Phe	Thr	
			20					25					30			
gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg																144
Val	Gly	Glu	Leu	Lys	Lys	Ala	Ile	Pro	Pro	His	Cys	Phe	Lys	Arg	Ser	
			35				40						45			
atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc																192
Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Ile	Trp	Asp	Ile	Ile	Ile	Ala	Ser	
			50				55					60				
tgc ttc tac tac gtc gcc acc act tac ttc cct ctc ctc cct cac cct																240
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Thr	Tyr	Phe	Pro	Leu	Leu	Pro	His	Pro	
			65				70				75				80	
ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc caa ggg tgc gtc																288
Leu	Ser	Tyr	Phe	Ala	Trp	Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys	Val	
				85					90					95		
cta acc ggc gtc tgg gtc ata gcc cac gag tgc ggc cac cac gcc ttc																336
Leu	Thr	Gly	Val	Trp	Val	Ile	Ala	His	Glu	Cys	Gly	His	His	Ala	Phe	
			100					105					110			
agc gac tac cag tgg ctt gac gac acc gtc ggt ctc atc ttc cac tcc																384
Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Leu	Ile	Phe	His	Ser	
			115				120						125			
ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cga cgc cac																432
Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg	His	
			130				135					140				

cat His 145	tcc Ser	aac Asn	act Thr	ggc Gly	tcc Ser 150	ctc Leu	gag Glu	aga Arg	gac Asp	gaa Glu 155	gtg Val	ttt Phe	gtc Val	ccc Pro	aag Lys 160	480
aag Lys	aag Lys	tca Ser	gac Asp	atc Ile 165	aag Lys	tgg Trp	tac Tyr	ggc Gly	aag Lys 170	tac Tyr	ctc Leu	aac Asn	aac Asn	cct Pro 175	ttg Leu	528
gga Gly	cgc Arg	acc Thr	gtg Val 180	atg Met	tta Leu	acg Thr	gtt Val 185	cag Gln	ttc Phe	act Thr	ctc Leu	ggc Gly 190	tgg Trp	ccg Pro	ttg Leu	576
tac Tyr	tta Leu	gcc Ala 195	ttc Phe	aac Asn	gtc Val	tcg Ser	gga Gly 200	aga Arg	cct Pro	tac Tyr	gac Asp	ggc Gly 205	ggc Gly	ttc Phe	gct Ala	624
tgc Cys	cat His 210	ttc Phe	cac His	ccc Pro	aac Asn	gct Ala 215	ccc Pro	atc Ile	tac Tyr	aac Asn	gac Asp 220	cgc Arg	gag Glu	cgt Arg	ctc Leu	672
cag Gln 225	ata Ile	tac Tyr	atc Ile	tcc Ser 230	gac Asp	gct Ala	ggc Gly	atc Ile	ctc Leu	gcc Ala 235	gtc Val	tgc Cys	tac Tyr	ggc Gly	ctc Leu 240	720
ttc Phe	cgt Arg	tac Tyr	gcc Ala 245	gcc Ala	gcg Ala	cag Gln	gga Gly	gtg Val 250	gcc Ala	tcg Ser	atg Met	gtc Val	tgc Cys	ttc Phe 255	tac Tyr	768
gga Gly	gtc Val	ccg Pro	ctt Leu 260	ctg Leu	att Ile	gtc Val	aat Asn	ggc Gly 265	ttc Phe	ctc Leu	gtg Val	ttg Leu	atc Ile 270	act Thr	tac Tyr	816
ttg Leu	cag Gln 275	cac His	acg Thr	cat His	cct Pro	tcc Ser	ctg Leu 280	cct Pro	cac His	tac Tyr	gat Asp	tcg Ser 285	tcc Ser	gag Glu	tgg Trp	864
gat Asp	tgg Trp 290	ttg Leu	agg Arg	gga Gly	gct Ala	ttg Leu 295	gct Ala	acc Thr	gtt Val	gac Asp	aga Arg	gac Asp	tac Tyr	gga Gly	atc Ile	912
ttg Leu 305	aac Asn	aag Lys	gtc Val	ttc Phe 310	cac His	aat Asn	att Ile	acc Thr	gac Asp	acg Thr 315	cac His	gtg Val	gcg Ala	cat His	cat His 320	960
ctg Leu	ttc Phe	tcc Ser	acg Thr 325	atg Met	ccg Pro	cat His	tat Tyr	cac His	gcg Ala 330	atg Met	gaa Glu	gct Ala	acc Thr 335	aag Lys	gcg Ala	1008
ata Ile	aag Lys	ccg Pro	ata Ile 340	ctg Leu	gga Gly	gag Glu	tat Tyr 345	tat Tyr	cag Gln	ttc Phe	gat Asp	ggg Gly 350	acg Thr	ccg Pro	gtg Val	1056

gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg 1104  
 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro  
           355                                  360                                  365

gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta 1152  
 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu  
           370                                  375                                  380

tga 1155

<210> 14

<211> 384

<212> PRT

<213> Brassica napus

<400> 14

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser  
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 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr  
                                   20                                  25                                  30  
 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser  
                                   35                                  40                                  45  
 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser  
                                   50                                  55                                  60  
 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro  
                                   65                                  70                                  75                                  80  
 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val  
                                   85                                  90                                  95  
 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe  
                                   100                                  105                                  110  
 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser  
                                   115                                  120                                  125  
 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His  
                                   130                                  135                                  140  
 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys  
                                   145                                  150                                  155                                  160  
 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu  
                                   165                                  170                                  175  
 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu  
                                   180                                  185                                  190  
 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala  
                                   195                                  200                                  205  
 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu  
                                   210                                  215                                  220  
 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu  
                                   225                                  230                                  235                                  240  
 Phe Arg Tyr Ala Ala Ala Gln Gly Val Ala Ser Met Val Cys Phe Tyr  
                                   245                                  250                                  255  
 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr  
                                   260                                  265                                  270  
 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp  
                                   275                                  280                                  285  
 Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile

290		295		300
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His				
305		310		315
Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala				
	325		330	335
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val				
	340		345	350
Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro				
	355		360	365
Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu				
370		375		380

<210> 15  
 <211> 1155  
 <212> DNA  
 <213> Brassica napus

<220>  
 <221> CDS  
 <222> (1)...(1152)

<400> 15	
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Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser	
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 gaa acc gac acc atc aag cgc gta ccc tgc gag aca ccg ccc ttc act	96
Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr	
20 25 30	
 gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg	144
Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser	
35 40 45	
 atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc	192
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser	
50 55 60	
 tgc ttc tac tac gtc gcc acc act tac ttc cct ctc ctc cct cac cct	240
Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro	
65 70 75 80	
 ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc caa ggg tgc gtc	288
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val	
85 90 95	
 cta acc ggc gtc tgg gtc ata gcc cac gag tgc ggc cac cac gcc ttc	336
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe	
100 105 110	
 agc gac tac cag tgg ctt gac gac acc gtc ggt ctc atc ttc cac tcc	384
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser	
115 120 125	

ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cga cgc cac	432
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His	
130 135 140	
cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag	480
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	
145 150 155 160	
aag aag tca gac atc aag tgg tac ggc aag tac cac aac aac cct ttg	528
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr His Asn Asn Pro Leu	
165 170 175	
gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg ccg ttg	576
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu	
180 185 190	
tac tta gcc ttc aac gtc tcg gga aga cct tac gac ggc ggc ttc gct	624
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala	
195 200 205	
tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgc gag cgt ctc	672
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu	
210 215 220	
cag ata tac atc tcc gac gct ggc atc ctc gcc gtc tgc tac ggt ctc	720
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	
225 230 235 240	
ttc cgt tac gcc gcc gcg cag gga gtg gcc tcg atg gtc tgc ttc tac	768
Phe Arg Tyr Ala Ala Ala Gln Gly Val Ala Ser Met Val Cys Phe Tyr	
245 250 255	
gga gtc ccg ctt ctg att gtc aat ggt ttc ctc gtg ttg atc act tac	816
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr	
260 265 270	
ttg cag cac acg cat cct tcc ctg cct cac tac gat tcg tcc gag tgg	864
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp	
275 280 285	
gat tgg ttg agg gga gct ttg gct acc gtt gac aga gac tac gga atc	912
Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile	
290 295 300	
ttg aac aag gtc ttc cac aat att acc gac acg cac gtg gcg cat cat	960
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	
305 310 315 320	
ctg ttc tcc acg atg ccg cat tat cac gcg atg gaa gct acc aag gcg	1008
Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala	
325 330 335	



ata aag ccg ata ctg gga gag tat tat cag ttc gat ggg acg ccg gtg	1056
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val	
340 345 350	

gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg	1104
Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro	
355 360 365	

gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta	1152
Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu	
370 375 380	

tga	1155
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<210> 16

<211> 384

<212> PRT

<213> Brassica napus

<400> 16

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20 25 30	
Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser	
35 40 45	
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser	
50 55 60	
Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro	
65 70 75 80	
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val	
85 90 95	
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe	
100 105 110	
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser	
115 120 125	
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His	
130 135 140	
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	
145 150 155 160	
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr His Asn Asn Pro Leu	
165 170 175	
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu	
180 185 190	
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala	
195 200 205	
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu	
210 215 220	
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	
225 230 235 240	
Phe Arg Tyr Ala Ala Ala Gln Gly Val Ala Ser Met Val Cys Phe Tyr	
245 250 255	
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr	

	260		265		270										
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp
	275						280					285			
Asp	Trp	Leu	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile
	290						295					300			
Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His
305					310					315					320
Leu	Phe	Ser	Thr	Met	Pro	His	Tyr	His	Ala	Met	Glu	Ala	Thr	Lys	Ala
				325					330					335	
Ile	Lys	Pro	Ile	Leu	Gly	Glu	Tyr	Tyr	Gln	Phe	Asp	Gly	Thr	Pro	Val
			340					345					350		
Val	Lys	Ala	Met	Trp	Arg	Glu	Ala	Lys	Glu	Cys	Ile	Tyr	Val	Glu	Pro
	355						360					365			
Asp	Arg	Gln	Gly	Glu	Lys	Lys	Gly	Val	Phe	Trp	Tyr	Asn	Asn	Lys	Leu
	370					375						380			

&lt;210&gt; 17

&lt;211&gt; 1155

&lt;212&gt; DNA

&lt;213&gt; Brassica napus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1152)

&lt;400&gt; 17

atg	ggt	gca	ggt	gga	aga	atg	caa	gtg	tct	cct	ccc	tcc	aag	aag	tct	48
Met	Gly	Ala	Gly	Gly	Arg	Met	Gln	Val	Ser	Pro	Pro	Ser	Lys	Lys	Ser	
1				5					10					15		
gaa	acc	gac	acc	atc	aag	cgc	gta	ccc	tgc	gag	aca	ccg	ccc	ttc	act	96
Glu	Thr	Asp	Thr	Ile	Lys	Arg	Val	Pro	Cys	Glu	Thr	Pro	Pro	Phe	Thr	
			20					25					30			
gtc	gga	gaa	ctc	aag	aaa	gca	atc	cca	ccg	cac	tgt	ttc	aaa	cgc	tcg	144
Val	Gly	Glu	Leu	Lys	Lys	Ala	Ile	Pro	Pro	His	Cys	Phe	Lys	Arg	Ser	
		35					40					45				
atc	cct	cgc	tct	ttc	tcc	tac	ctc	atc	tgg	gac	atc	atc	ata	gcc	tcc	192
Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Ile	Trp	Asp	Ile	Ile	Ile	Ala	Ser	
	50					55					60					
tgc	ttc	tac	tac	gtc	gcc	acc	act	tac	ttc	cct	ctc	ctc	cct	cac	cct	240
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Thr	Tyr	Phe	Pro	Leu	Leu	Pro	His	Pro	
65					70				75					80		
ctc	tcc	tac	ttc	gcc	tgg	cct	ctc	tac	tgg	gcc	tgc	caa	ggg	tgc	gtc	288
Leu	Ser	Tyr	Phe	Ala	Trp	Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys	Val	
				85					90					95		
cta	acc	ggc	gtc	tgg	gtc	ata	gcc	cac	gag	tgc	ggc	cac	cac	gcc	ttc	336
Leu	Thr	Gly	Val	Trp	Val	Ile	Ala	His	Glu	Cys	Gly	His	His	Ala	Phe	
			100					105						110		

agc gac tac cag tgg ctt gac gac acc gtc ggt ctc atc ttc cac tcc	384
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser	
115 120 125	
ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cga cgc cac	432
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His	
130 135 140	
cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag	480
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	
145 150 155 160	
aag aag tca gac atc aag tgg tac ggc aag tac ctc aac aac cct ttg	528
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu	
165 170 175	
gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg ccg ttg	576
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu	
180 185 190	
tac tta gcc ttc aac gtc tcg gga aga cct tac gac ggc ggc ttc gct	624
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala	
195 200 205	
tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgc gag cgt ctc	672
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu	
210 215 220	
cag ata tac atc tcc gac gct ggc atc ctc gcc gtc tgc tac ggt ctc	720
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	
225 230 235 240	
ttc cgt tac gcc gcc gcg cag gga gtg gcc tcg atg gtc tgc ttc tac	768
Phe Arg Tyr Ala Ala Ala Gln Gly Val Ala Ser Met Val Cys Phe Tyr	
245 250 255	
gga gtc ccg ctt ctg att gtc aat ggt ttc ctc gtg ttg atc act tac	816
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr	
260 265 270	
ttg cag cac acg cat cct tcc ctg cct cac tac gat tcg tcc gag tgg	864
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp	
275 280 285	
gat tgg ttg agg gga gct ttg gct acc gtt gac aga gac tac gaa atc	912
Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Glu Ile	
290 295 300	
ttg aac aag gtc ttc cac aat att acc gac acg cac gtg gcg cat cat	960
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	
305 310 315 320	

ctg ttc tcc acg atg ccg cat tat cac gcg atg gaa gct acc aag gcg	1008
Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala	
325 330 335	
ata aag ccg ata ctg gga gag tat tat cag ttc gat ggg acg ccg gtg	1056
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val	
340 345 350	
gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg	1104
Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro	
355 360 365	
gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta	1152
Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu	
370 375 380	
tga	1155

&lt;210&gt; 18

&lt;211&gt; 384

&lt;212&gt; PRT

&lt;213&gt; Brassica napus

&lt;400&gt; 18

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser	
1 5 10 15	
Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr	
20 25 30	
Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser	
35 40 45	
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser	
50 55 60	
Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro	
65 70 75 80	
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val	
85 90 95	
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe	
100 105 110	
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser	
115 120 125	
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His	
130 135 140	
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	
145 150 155 160	
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu	
165 170 175	
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu	
180 185 190	
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala	
195 200 205	
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu	
210 215 220	
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	

225		230		235		240									
Phe	Arg	Tyr	Ala	Ala	Ala	Gln	Gly	Val	Ala	Ser	Met	Val	Cys	Phe	Tyr
			245						250					255	
Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Gly	Phe	Leu	Val	Leu	Ile	Thr	Tyr
			260						265					270	
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp
			275						280					285	
Asp	Trp	Leu	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Glu	Ile
			290						295					300	
Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His
305							310				315				320
Leu	Phe	Ser	Thr	Met	Pro	His	Tyr	His	Ala	Met	Glu	Ala	Thr	Lys	Ala
							325				330				335
Ile	Lys	Pro	Ile	Leu	Gly	Glu	Tyr	Tyr	Gln	Phe	Asp	Gly	Thr	Pro	Val
			340						345					350	
Val	Lys	Ala	Met	Trp	Arg	Glu	Ala	Lys	Glu	Cys	Ile	Tyr	Val	Glu	Pro
			355						360					365	
Asp	Arg	Gln	Gly	Glu	Lys	Lys	Gly	Val	Phe	Trp	Tyr	Asn	Asn	Lys	Leu
			370						375					380	

<210> 19  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 19  
 ggatatgatg atggtgaaaag a

21

<210> 20  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 20  
 tctttcacca tcatcatatc c

21

<210> 21  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 21  
 gttatgaagc aaagaagaaa c

21

<210> 22

<211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 22  
 gtttcttctt tgctttgctt cataac 26

<210> 23  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 23  
 caucaucauc aucttcttcg tagggttcat cg 32

<210> 24  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 24  
 cuacuacuac uatcatagaa gagaaagggtt cag 33

<210> 25  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 25  
 caucaucauc aukatgggtg cacgtggaag aa 32

<210> 26  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 26  
 cuacuacuac uatctttcac catcatcata tcc 33

<210> 27  
 <211> 30  
 <212> PRT  
 <213> *Arabidopsis thaliana*

<400> 27  
 Ile Trp Val Ile Ala His Glu Cys Gly His His Ala Phe Ser Asp Tyr  
   1                  5                  10                  15  
 Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser Phe  
                   20                  25                  30

<210> 28  
 <211> 30  
 <212> PRT  
 <213> *Glycine max*

<400> 28  
 Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe Ser Lys Tyr  
   1                  5                  10                  15  
 Gln Trp Val Asp Asp Val Val Gly Leu Thr Leu His Ser Thr  
                   20                  25                  30

<210> 29  
 <211> 30  
 <212> PRT  
 <213> *Zea mays*

<400> 29  
 Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe Ser Asp Tyr  
   1                  5                  10                  15  
 Ser Leu Leu Asp Asp Val Val Gly Leu Val Leu His Ser Ser  
                   20                  25                  30

<210> 30  
 <211> 29  
 <212> PRT  
 <213> *Ricinus communis*

<400> 30  
 Trp Val Met Ala His Asp Cys Gly His His Ala Phe Ser Asp Tyr Gln  
   1                  5                  10                  15  
 Leu Leu Asp Asp Val Val Gly Leu Ile Leu His Ser Cys  
                   20                  25

<210> 31  
 <211> 29  
 <212> PRT  
 <213> *Arabidopsis thaliana*

<400> 31  
 Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His His  
   1                  5                  10                  15  
 Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val

20

25

<210> 32  
 <211> 29  
 <212> PRT  
 <213> Glycine max

<400> 32  
 Leu Leu Val Pro Tyr Phe Ser Trp Lys Ile Ser His Arg Arg His His  
   1                  5                  10                  15  
 Ser Asn Thr Gly Ser Leu Asp Arg Asp Glu Val Phe Val  
                   20                  25

<210> 33  
 <211> 29  
 <212> PRT  
 <213> Zea mays

<400> 33  
 Leu Met Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His His  
   1                  5                  10                  15  
 Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val  
                   20                  25

<210> 34  
 <211> 29  
 <212> PRT  
 <213> Ricinus communis

<400> 34  
 Leu Leu Val Pro Tyr Phe Ser Trp Lys His Ser His Arg Arg His His  
   1                  5                  10                  15  
 Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val  
                   20                  25

<210> 35  
 <211> 36  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 35  
 Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His Asn Ile Thr Asp  
   1                  5                  10                  15  
 Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr Asn Ala  
                   20                  25                  30  
 Met Glu Ala Thr  
                   35

<210> 36  
 <211> 36  
 <212> PRT  
 <213> Glycine max



&lt;400&gt; 36

Asp	Arg	Asp	Tyr	Gly	Ile	Leu	Asn	Lys	Val	Phe	His	His	Ile	Thr	Asp
1				5					10					15	
Thr	His	Val	Ala	His	His	Leu	Phe	Ser	Thr	Met	Pro	His	Tyr	His	Ala
			20					25					30		
Met	Glu	Ala	Thr												
			35												

&lt;210&gt; 37

&lt;211&gt; 36

&lt;212&gt; PRT

&lt;213&gt; Zea mays

&lt;400&gt; 37

Asp	Arg	Asp	Tyr	Gly	Ile	Leu	Asn	Arg	Val	Phe	His	Asn	Ile	Thr	Asp
1				5					10					15	
Thr	His	Val	Ala	His	His	Leu	Phe	Ser	Thr	Met	Pro	His	Tyr	His	Ala
			20					25					30		
Met	Glu	Ala	Thr												
			35												

&lt;210&gt; 38

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Ricinus communis

&lt;400&gt; 38

Asp	Arg	Asp	Tyr	Gly	Ile	Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp
1				5					10					15	
Thr	Gln	Val	Ala	His	His	Leu	Phe	Thr	Met	Pro					
			20					25							

&lt;210&gt; 39

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 39

Ile	Lys	Trp	Tyr	Gly	Lys	Tyr	Leu	Asn	Asn	Pro	Leu	Gly	Arg	Ile	Met
1				5					10					15	

&lt;210&gt; 40

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Glycine max

&lt;400&gt; 40

Val	Ala	Trp	Phe	Ser	Leu	Tyr	Leu	Asn	Asn	Pro	Leu	Gly	Arg	Ala	Val
1				5					10					15	

&lt;210&gt; 41

&lt;211&gt; 16

&lt;212&gt; PRT

<213> Zea mays

<400> 41

Pro Trp Tyr Thr Pro Tyr Val Tyr Asn Asn Pro Val Gly Arg Val Val  
 1 5 10 15

<210> 42

<211> 16

<212> PRT

<213> Ricinus communis

<400> 42

Ile Arg Trp Tyr Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg Ile Met  
 1 5 10 15

<210> 43

<211> 22

<212> PRT

<213> Arabidopsis thaliana

<400> 43

Trp Ala Leu Phe Val Leu Gly His Asp Cys Gly His Gly Ser Phe Ser  
 1 5 10 15  
 Asn Asp Pro Lys Leu Asn  
 20

<210> 44

<211> 22

<212> PRT

<213> Brassica napus

<400> 44

Trp Ala Leu Phe Val Leu Gly His Asp Cys Gly His Gly Ser Phe Ser  
 1 5 10 15  
 Asn Asp Pro Arg Leu Asn  
 20

<210> 45

<211> 22

<212> PRT

<213> Glycine max

<400> 45

Trp Ala Leu Phe Val Leu Gly His Asp Cys Gly His Gly Ser Phe Ser  
 1 5 10 15  
 Asn Asn Ser Lys Leu Asn  
 20

<210> 46

<211> 22

<212> PRT

<213> Arabidopsis thaliana

&lt;400&gt; 46

Trp Ala Ile Phe Val Leu Gly His Asp Cys Gly His Gly Ser Phe Ser  
 1 5 10 15  
 Asp Ile Pro Leu Leu Asn  
 20

&lt;210&gt; 47

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; exemplary motif

&lt;400&gt; 47

Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val  
 1 5 10

&lt;210&gt; 48

&lt;211&gt; 22

&lt;212&gt; PRT

&lt;213&gt; Glycine max

&lt;400&gt; 48

Trp Ala Leu Phe Val Leu Gly His Asp Cys Gly His Gly Ser Phe Ser  
 1 5 10 15  
 Asp Ser Pro Pro Leu Asn  
 20

&lt;210&gt; 49

&lt;211&gt; 29

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 49

Ile Leu Val Pro Tyr His Gly Trp Arg Ile Ser His Arg Thr His His  
 1 5 10 15  
 Gln Asn His Gly His Val Glu Asn Asp Glu Ser Trp His  
 20 25

&lt;210&gt; 50

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; exemplary motif

&lt;400&gt; 50

Asp Arg Asp Tyr Glu Ile Leu Asn Lys Val  
 1 5 10

&lt;210&gt; 51

<211> 29  
 <212> PRT  
 <213> Glycine max

<400> 51  
 Ile Leu Val Pro Tyr His Gly Trp Arg Ile Ser His Arg Thr His His  
           1                  5                  10                  15  
 Gln His His Gly His Ala Glu Asn Asp Glu Ser Trp His  
                   20                  25

<210> 52  
 <211> 29  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 52  
 Ile Leu Val Pro Tyr His Gly Trp Arg Ile Ser His Arg Thr His His  
           1                  5                  10                  15  
 Gln Asn His Gly His Val Glu Asn Asp Glu Ser Trp Val  
                   20                  25

<210> 53  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> exemplary motif

<400> 53  
 Lys Tyr His Asn Asn Pro  
           1                  5

<210> 54  
 <211> 29  
 <212> PRT  
 <213> Glycine max

<400> 54  
 Ile Leu Val Pro Tyr His Gly Trp Arg Ile Ser His Arg Thr His His  
           1                  5                  10                  15  
 Gln Asn His Gly His Ile Glu Lys Asp Glu Ser Trp Val  
                   20                  25

<210> 55  
 <211> 6  
 <212> PRT  
 <213> Brassica napus

<400> 55  
 Gly His Asp Cys Ala His  
           1                  5

<210> 56

<211> 6  
 <212> PRT  
 <213> Brassica napus

<400> 56  
 Gly His Lys Cys Gly His  
     1                    5

<210> 57  
 <211> 6  
 <212> PRT  
 <213> Brassica napus

<220>  
 <221> VARIANT  
 <223> amino acid residues 94-99 of Canola-Fad3

<400> 57  
 Gly His Asp Cys Gly His  
     1                    5

<210> 58  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> exemplary motif

<400> 58  
 His Lys Cys Gly His  
     1                    5

<210> 59  
 <211> 12  
 <212> DNA  
 <213> Phaseolus vulgaris

<400> 59  
 tgggtcttttg gt

12

<210> 60  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> exemplary motif

<400> 60  
 His Glu Cys Gly His  
     1                    5

<210> 61

<211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> exemplary motif

<400> 61  
 His Arg Arg His His  
       1                  5

<210> 62  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> exemplary motif

<400> 62  
 His Arg Thr His His  
       1                  5

<210> 63  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> exemplary motif

<400> 63  
 His Val Ala His His  
       1                  5

<210> 64  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> exemplary motif

<400> 64  
 Lys Tyr Leu Asn Asn Pro  
       1                  5

<210> 65  
 <211> 29  
 <212> PRT  
 <213> Brassica napus

<400> 65  
 Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe Ser Asp Tyr

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<400> 66
Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His Asn Ile Thr Asp
  1             5             10             15
Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala
          20             25             30
Met Glu Ala Thr
          35

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<400> 67
Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu Gly Arg Thr Val
  1             5             10            15
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<220>
<223> exemplary motif
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<210> 69
<211> 6
<212> PRT
<213> Artificial Sequence
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```
<400> 69
Ala His Glu Cys Gly His
  1               5
```

<210> 70  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> exemplary motif

<400> 70  
His Asp Cys Gly His  
1 5